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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISI REFERENCE AUTHORS TITLE JOURNAL FEATURES	RESULT 1 166494 LOCUS DEFINITION ACCESSION VERSION VERSION		4 4 5 4	C 43	4.4	0 0 40	υ	37	υ	w		C (3)	מי	28	26	c 25	o N		20	c 19	 		0 C	. سر،					σ	n 4. v	ω		Result
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Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
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                                                                                                                                                                                                                           Blanton,R.L., Fuller,D., Iranfar,N., Grimson,M.J. and Loomis,W.F. The cellulose synthase gene of Dictyostelium Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2391-2396 (2000)
                                                                                                                                                                                                                                                                                                                                                                                     AF163835
Dictyostelium
                                                                                                                          Submitted (29-JUN-1999) Center for Gilman Drive, La Jolla, CA 92093, U
                                                                                                                                                      Blanton, R.L., Fuller, D., Direct Submission
                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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          /gene="dcsA"
806. .3985
                                                                 organism="Dictyostelium/strain="AX4"
                                                                                                             Location/Qualifiers
                                                  db_xref="taxon:44689"
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11.0%; Pred. No. 1
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ilarity 45.8%;
Conservative
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$RNLKPKP$Q$NLKWIARDLKKK$VRKD$ERKLK$SGVLKKKNTVMDFGEDDGGSGDD
GNITEGLPI$EGMDDLP$$$NSRGGSGNDEQKKQFPKEMN$P$$EYGTT$GGQRFDTL
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HAHNI VLELVLGELVLLEVDVKVCI PRVG"
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/product="cellulose synt)
/protein_id="AAF00200.1"
/db_xref="GI:6002921"
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Pred. No. 2.9;
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Rickettsia prowazekii

Hinxton,

Cambridgeshire,

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    JOURNAL
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                                                                                                                                             195829 bp DNA
Human DNA sequence from clone RP5-1087E8
1942:11-42:2, complete sequence.
AL353689
 Direct Submission
Submitted (19-OCT-2001)
                              Moore, M
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 195829)
                                                                                          Homo sapiens
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Uppsala, SWEDEN
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Biology, Husargatan 3,
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Andersson, S.G.E.
Direct Submission
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1 (bases 1 to 441)
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/strain="Madrid E"
/db xeef="taxon:782"
/clone="M340R"
/clone lib="genomic DNA, J. B/
177:4171-4175(1995)"
. a 57 c 37 g 155 t
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Genomics 1 (4), 293-315 (1996)
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Sanger Centre,
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                                                                         Euteleostomi;
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                                                                                                                                                                                                551 CACAATCTGGTGACCAAGTCAACAAGGATATCACTCAAAAATATAGAACCATTTTGGATT
                                                                        611 CAACAGTTGTTGCCTCTCAAAGAGAATATATTAACTCTGTAAAGCAAGGTAAACCAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
http://www.sanger.ac.uk/HGP/Chrl
RP5-1087E8 is from the library RPCI-5 constructed by the group Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 21, 2001 this sequence version replaced gi:15983876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
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During sequence assembly data is compared from overlapping clones
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                                                                                                                                                                                                                                                                                                                                                                                                                    57449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Sequence from overlapping clone RP11-375H24
(AL391628). Assembly confirmed by restriction digest."
39840. .39867
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13995. .14136
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restriction digest data."
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be_approximately 250bp by restriction
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Pred. No. 3.9;
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CE 2 (bases 1 to 146568)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Reckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Anderson, S., Baldwin, J., Barna, N., Becwan, A., Burkett, G., Castle, A., Chcepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Chcepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Hotton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Hotton, L., Gardyna, S., Lehoczky, J., Levine, R., Leu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Luc, G., Liu, G., Locke, K., Landers, T., Lehoczky, J., McDes, C., Kann, L., Karatas, A., Klein, J., McPheeters, R., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zimmer, A. and S., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 1, 2000 this sequence version replaced gi:6910657. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
* NOTE: This is a 'working draft' sequence. It current * consists of 12 contigs. The true order of the pieces
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Homo sapiens clone RP11-28H7, WORKING DRAFT SEQUENCE, 12 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                             Center project name: L4767

Center clone name: 28 H 7

Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 140377 bases at least Q30 Consensus quality: 143582 bases at least Q30 Consensus quality: 143644 bases at least Q20 Insert size: 14500; agarose-fp Insert size: 145468; sum-of-contigs Quality coverage: 4.8 in Q20 bases; sum-of-contigs Quality coverage: 4.8 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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Db 118836
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Best Local
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CACAGAAATGCACATCAAAACTACAATGAGATATCATCTCACCCCAGTTAAAATGGCTTA 118895
                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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9074 9173: gap of 100 bp
9174 16904: contig of 7731
16905 17004: gap of 100 bp
17005 25601
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115547 115646:
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                                                                   Conservative
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25702 3447
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115647. .146568
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69081. .84607
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55533. .68980
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25702. .34479
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7 146568: contig of 30922
Location/Qualifiers
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101026. .115546
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/db_xref="taxon:9606"
/clone="RP11-28H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_fragment"
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41772: contig of 7193 k
41872: gap of 100 bp
55432: contig of 13560
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25601: contig of 8597 bp
5701: gap of 100 bp
34479: contig of 8778 bp
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3: gap of 100 bp
9073: contig of 6690 bp in length
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RES NUZITY, D.M., Kodmis, C., ACI, C., ACE, J. R., BATKSTT., BATEST, C., ALIEUK, J., BATKSTT., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTG
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1 (bases 1 to 165236)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J.,
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STSs are identified using ePCR (Genome Res. 7:541-550) sea of a local database that includes entries from dbSTS, GDB, an local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are no identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entire insert of this clone. Overlapping regions contine insert of this clone, so the sequence for the remainder sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-FEB-2000) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 165236)
                                                                                                                                                                                                       Position
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Direct Submission
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contig length:
Phrap values in estimate:
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gtgcaggcac (n) acaaaaaaag tttaaagttt (n) Attctttctt tgtctccatg (n) cacaatttct acattctgaa (n) tactgggcac cagcctggcc (n) acatggtgaa tttgttttgg (n) tttaaaaac tttgttttag (n) catccattgt caaagcaagt (n) acatggaact caaagcaagt (n) acatggaact
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complement (8266. .8568)
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7428. .7874
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2705. .5433
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                       /rpt_family="(TAA)n"
7980. .8265
                                                  /rpt_family="L1MCc"
7960. .7979
                                                                                   rpt_family="L1"
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/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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GCATAGTTTTGTTTCCTCAAGTGCCTCTGTCAATGGTTTCCGTTTATGGTTTCCCACAATA
                               RRTRHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWWTRTNNNNNNNNNNNNACRNTRT
                                                             TTCTTTGGGTGGTGTCAAGAGTTTGGATGAATCATTGGTTCGTGGTGTTACTGGTGATTT
                                                                                             AGKMCNNNNNWTTDVRRMAMKAKNNNNNNAYWTACYNRAATNNKMATHWMKWTHGAHSK
                                                                                                                           TAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTTCCCTTCCATATCTTGT
                                                                                                                                                            AKSCATNNAMWYATTRWAAYAAAKWARWAGNNMRMYGAAAGNKWGCMAAMATMGBWWADT
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N. Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 174253)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-131K16
                                                                                                                                                                                                                                                                                                                              AC068590.2 GI:8389591
HTG; HTGS_PHASE1; HTGS_DRAFT
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WORKING DRAFT
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REFERENCE

AUTHORS

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Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Viene, Subriasion, J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 9, 2000 this sequence version replaced gi:7705204. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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3 (bases 1
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                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: L9496
Center clone name: 131 K 16
Center clone name: 131 K 16
Center clone name: 131 K 16
Sequencing vector: M13, M79815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 156518 bases at least Q40
Consensus quality: 165902 bases at least Q30
Consensus quality: 165336 bases at least Q20
                                                                                                                                                                                                                                                                                                                                               Insert size: 170000; agarose-fp
Insert size: 171333; sum-of-contigs
Quality coverage: 3.5 in Q20 bases;
Quality coverage: 3.5 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
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sum-of-contigs
                                                                                                                   are unknown.
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                                                                                                               misc_feature
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117424 117523:
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18336 18435:
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/note="assembly_fragment"
                                                                       note="assembly_fragment"
                                                                                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
|db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation
                                                                                                                                                                                                                                                                           clone="RP11-131K16"
                                                                                                                                                                                                                                                                                                                                                       chromosome="8"
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7753: co
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5/638: contig of 5148 bp ii
77738: gap of 100 bm
65255: contin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9255: gap of 10

88577: contig of 10

18677: gap of 10

98500: contig of 9

106888: contig of 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2674: gap of 100 bp
36983: contig of 4309 bp
7083: gap of 100 bp
4157: contig of 4474 bp
1657: gap of 100 bp
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117423: cc
7527
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19919: contig of 1484 k
0019: gap of 100 bp
22351: contig of 2332 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79155: cont
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46775: contig of 5
5875: gap of 10
52390: contig of 5
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154901: cont
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137392: contig of 11301
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125991: cont
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9492: con
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5627:
                                                                                                                                                                                                                                   lib="RPCI-11 Human Male BAC"
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ap of 100 bp
contig of 3022 bp
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                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187254)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, Clone RP11-2318
Unpublished
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.
                                                                                                                                                                                                                                                                          AC124649 187254 bp DNA linea Homo sapiens chromosome 8 clone RP11-2318 map 8, PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                             AC124649.3 GI:22123145
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46876. .52390
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37084. .41557
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28293. .32574
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25574. .28192
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22452. .25473
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13279. .15953
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7854. .9492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 2; Length 174253; Pred. No. 9;
                                                                                                                                                                                                                                                                                               *** SECHENCTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DE 3 (bases 1 to 187254)

Sirren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Chara, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camaratta, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Lindbers, T., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McMindy, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zodv, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:21699345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                       This sequence will be replaced by the finished sequence as soon as it is available the accession number will be preserved.

64780: contig of 64780 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center_project name: L27405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 23_I_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                         64781 64880: gap of 100 bp
64881 187254: contig of 122374 bp in length
                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zimmer, A. and Zody, M.
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Best Local Similarity
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Allen, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banke, T., Barbaria, J., Benton, J., Biange, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkett, C., Burrell, K.L., Byrd, N.C., C., C., C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., C., Carron, T.F., Carter, M., Caracos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Ceveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgard, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Garza, N., Gill, R., Gorrell, J.H., Gaerar, M., Gunarratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Jackbson, B., Jia, Y., Johnson, R., Jollvet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Lucier, R., Luna, R., Ma, J., Lotharge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lucier, R., Lucier, R., Luna, R., Martinez, E., Massey, E., McLeod, M.P., Meador, M., Majus, P., Martinez, E., Massey, E., McLeod, M.P., Meador, M., Majus, M., Martinez, E., Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCAATTTCAAACTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGATAT 719
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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unordered pieces.
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/clone="RP11-2318"
/clone lib="RPCI-11 Human Male BAC"
/clone lib="RPCI-11 Human Male BAC"
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2002 this sequence version replaced gi:17973311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 195912)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a "working draft" sequence. It currently consists of 57 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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be preserved
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 148958 bases at least Q40
Consensus quality: 154477 bases at least Q30
Consensus quality: 158706 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: hgsc-help@bcm.tmc.edu
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                                               Direct Submission
Submitted (15-AUG-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA
On Jul 9, 2002 this sequence version replaced gi:21672150.
                                                                                                                              Submitted (20-JUN-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
3 (bases 1 to 114741)
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kin, D. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                 Shaull,S., Lin,S., Dixon,R., May,G., Sur Cook,D., Kim,D. and Roe,B.A. Medicago truncatula BAC Clone mth1-10g9
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Center: Department Of Chemistry
The University Of Oklahoma
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Shaull,S., Lin,S., Dixon,R., May,G.,
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g of 5688 bp in length
g of 5680 bp in length
g of 9320 bp in length
                   And
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WORKING DRAFT SEQUENCE, 5
                                                                                                                                                                                                                                                                     Sumner, L., Gonzales, B
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Center code: UOKNOR

NOTE: This is a 'working draft' sequence. It currently

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
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the accession number will be preserved.

the accession number will be preserved.

3390 389: contig of 3389 bp in length

3390 3489: gap of unknown length

19780 19879: gap of unknown length

1980 39080: contig of 19201 bp in length

39180 39980: gap of unknown length

39181 39180: gap of unknown length

67047 67146: gap of unknown length

67047 117741: contig of 47595 bp in length.
                                                                                                                                                                                         1 (bases 1 to 282610)
Andersson,S.G., Zomorodipour,A., Andersson,J.O.,
Sicheritz-Ponten,T., Alsmark,U.C., Podowski,R.M.,
Eriksson,A.S., Winkler,H.H. and Kurland,C.G.
The genome sequence of Rickettsia prowazekii and t
  Direct Submission
Submitted (11-NOV-1998)
Siv.Andersson@molbio.uu
                                                                2 (bases 1 to 282610)
Andersson, S.G.E.
                                                                                                                                                                          mitochondria
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia; tyr
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This sequence will be replaced
  Andersson@molbio.uu.se, Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%;
ilarity 50.2%;
Conservative
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19145 c 18697 g 3
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Pred. No. 13;
0; Mismatches
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37461 t
                      Andersson,
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Biology, University
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                                                                                                                                                                                                                                                                                                         group.
                                                                                                                                                                                                                                        Naslund, A.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānsiation="mllnhskvfibitdgyvegidvhkraqgikhfflkkgyslspti
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afsvsifqnpoillldevfaagdsyfiekslnlmknkfkntpisiivshqebiikdnc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="mtkliihlusdssvqtakhaansalaqftsikqklyhmpmirng
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2837. .3724
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Location/Qualifiers
                                                                                                                                                                                                                                          INGSLPDMMLIIKSVIVAFITVFISYLIYRQFSKRVIYYL"
                                                                                                                                                                                                                                                                 AFLTPYIRDIPQMLNVILGVIYWSIPIVYPYSLIPESKKIYFEFNPFFLVIRPVQVLV
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                                                                                                                                                     gene="RP005"
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tränblation="MVAATGHRICNDCSKACIYOKQDPVNIFLIESNILEETLKLPYG
LEIYILUTRWNPLNIYAPLPKEFTNYNILVTGLGPAGFSLSYLLRSGHNVTAIDGLK
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IDNVPSFKGSYACFITQLDYLLTSRINKINILNDKTFELIIHSPLAAKNFQFGQFFRL
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TRIGEYSMIGGLSPVGADVIPFGLVSSKRAVLEGLNLIGMNRKGFDKADSLTALNAVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAVKKYPLEKIKDIDFEDVYLKITNLIGTNFTSREFAKQIVIWQQDEESFSLELDIAA
RYAAYRVFSYYNSLSSWNKNLFLQNDILFNLQQKLDKKNLIDDKKILKYQKNERVDFD
YKDSFFNLDEALNNSHYCIYCHKRDKDSCSKGFDVIPHFDRVISVDKIPRLSYRMTTG
complement (9267. .9339)
/gene="tRNA Phe (GAA)"
                                                                     QLVKTSNSKLKK"
                                                                                                 KYCALGGQVGIAGHLNIGDGTQVAAQGGVAQNIEEGKIVGGSPAVPIMDWHRQSIIMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (7659. .8699)
/gene="RP009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (7659.
/gene="RP009"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (7031. .7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6227. .7021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6227. .7021)
/gene="RP007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEIAEELQELKIFGENTELIINVNSLMQCMMKGICGQCIQKVKGKQKYIFACSEQNQN
VEIIDFKSLKTRLRQNSLQEKMSN"
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/protein_id="CAA14479.1"
/db_xref="GI:3860578"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="RP008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8699)
                                                                                                                                                                                                                                                                                                                                                                                                           GLUCOSAMINE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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Best Local S
Matches 128
                                      TITLE
                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTGGGTTAACCGTTTCAGTTCTTATTATAGGTATAGTGTCTATGGCTATAGGAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTAAGGATATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTTATGCTCAATTGAGCCAACAATT 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCGGATTAACTCTCCCAGCCAACAAGAATGGTATTGCTCATTTGGCTAAATCATCAAA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTTAGTTTTGGACTTGTTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAAATTTTTGAATTGGAATTTTTATTAATTAGATAATTGCTTTTAAAAAGCACAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCATACGTTTATACTGATGTTTTGGCTTTGAATTCCAATTTGTGTGATGAAAAGCAAAA 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTGATAAGAATTGAGCTTAAAACT 255103
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                                                                                                                                                                                              Staphylococcus aureus subsp. aureus MW2 (strain:MW2)
Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                              AP004829 304050
Staphylococcus aureus subsp.
strain:MW2, section 8/10.
AP004829 BA000033
                                  Yamamoto, K. and Hiramatsu, K. Genome and virulence determinants
                                                                                                 Nagai,Y.,
                                                                                                                                Baba, T., Takeuchi, F., Kuroda, M.,
                                                                                                                                                                                                                                                                                                                                     AP004829.1
   community-acquired MRSA
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/gene="RP012"
10683. .11756
/gene="RP012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKRILSFIFIILFFNSSYAVEKAAIITDYKPIFLPVITENKKIK
IAIRSYLKNKKSYFVLVDPNSFKTEIVLQELVILPANKIEKENLLIKLNKTSYIKALN
KYNFIDQSLQSFKQDEFSNKFTDNTIVYEHKLNSKSSHSSTFMNSTVQQNYGATSSMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLNYDIMLNFITIFMIKIGNIELSSNVILAPMSDVTDLEFRKLV
KREGAGLIVVSEMIASRAMIMKSRQSMQKCA IMHDDFTSACVQLAGCEPDVIAEAAKMN
EDMGAKIIDLNFGCPAKKVVGGYAGSALMRDGDLAAKIFBATVKAVKIPVTVKMRIGW
DDMTRNAFTLAKIAANSGVQMVTVHGBTRCQFYSGNANMDFIRTVKEAVKIPVIANGD
ITNFAKAKEALQRSGADGIMVGRGVYGKPWLISQIAYYLKTGKEKPAPSIAEQLDIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVMDANK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="NIFR3-LIKE PROTEIN (nifR3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (9267. .9339)
/gene="tRNA Phe (GAA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="unknown"
/protein_id="CAA14484.1"
/db_xref="GI:3860583"
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/db_xref="GI:3860582"
                                                                                          Iwama, N., Asano, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="RP011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="RP011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
table=11
                                                                                                                                                                                                                                                                                                                                         GI:21205117
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304050 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                      aureus MW2 DNA, complete genome,
                                                                                                 Naimi, T.,
                                                                                                                            Yuzawa, H.,
                               of high virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                    Kuroda, H.,
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                                                                                                                                   Aoki, K.,
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Gaps

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887

254956

255016

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Cui,L.,

Oguchi, A.

BCT 02-JUL-2002

gene

Sg

gene Sg

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PUBMED
REFERENCE
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                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 3: 22040717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aoki,K., Oguchi,A., Nagai,Y., Asano,K., Iwama,N.,Kuroda,M., Hiramatsu,K. and Kikuchi,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                              /translation="MSELTAKQARFVNEYIRTLNVTQSAIKAGYNANSAHVTACRLLK
KPHIKQYIQEQKDKIIDENVLTAKELLHVLTNATVGDETETKEVVVKRGEYKENPQSG
KVQLVYNEHVELIEVPIKPSDRLKAREMLGKYHKLFTDKHDINGNVPIFINIGEWDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (1932. .2522)
/gene="MW1949"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDNINKNEKFRVLSTIAITISFILNFGLFISLAIWSINSMGNKQ
CISLNLLLSDDTFAVISVMTTLGTAILGGIAPSIYGIFTSPIDKKSSFRAISDWEQEQ
RNNVKDLMMLLPFTLLSILIVIFIFQFAYSKLFNTIAIIIFIILVVMFFLILLICYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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HDDYFLLLLIKENKIIGLSGMCKMMFYEKNAEYMRILAFVIHSEFRKKGYGKRLLADS
EEFSKRLNCKAITLNSGNRNERLSAHKLYSDNGYVSNTSGFTKQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein, similar to acetyltransferase [Genomic island nu Sa 4mw]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (629. .1072)
/gene="MW1947"
                                                                                                                                                                                                                  complement (2519. .2734)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORFID:MW1949
hypothetical protein, similar to bacteriophage terminase
hypothetical protein, similar to bacteriophage terminase
hypothetical protein, similar to bacteriophage terminase
hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1932. .2522)
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                                                                                                                                          [Genomic island nu
                                                                                                                                                                                                                                        /gene="MW1950"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [Genomic island nu Sa 4mw]"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Staphylococcus aureus subsp. aureus MW2"
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                                                                                                                                                                                                                                                                 (2519. .2734)
                                                                                                                                               Sa 4mw]"
                                                                     protein"
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complement(5125, .5409)
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3072. .3338
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                                                                                                                                                                                   CTAAATCATCAAACTTTTATGCTCAATTGAGCCAACAATTCGATGCCAAGGAAAGTGAAG 994
                                                                                                                                                                                                                                                                                                                              ATCCAATTAATATAAAAATATCAAATCAAACACGTTGATAGATTAAAATTTTAAAAG
                                                                                                                                                                                                                                                                                                                                                             ATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                    GCATGCGTTATGATTTAAAGCTCTTCTTTTTTATATTTTATAAATTTTGTGAGCAAGCC 262431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGTATGTAGGTTGATAAGAAGAGTTTGAATGATAACTCATTGCATTTAAAGATAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGTATGTGTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGTGATAACGTTGAAATGTTTGTTGAATATGTAAAACAACATATGATAGTATAATGTC
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                                                                                          TTAGAGTTTTGAGATGTGTTGACTTTG 1021
                                                                                                                                        CTTAAACATCAAATTATTATAAGAAATAAATGTATTTAACCATATTCTAGTAATAAAAAT 262251
                                                                                                                                                                                                                                   TTTACATATCAGTTAAGATACAAAATATTCAGACTAATAATTTTCAATTTGGCAAAATAT 262311
                                                                                                                                                                                                                                                                              TGGACTTGTTGGGTCTCGGATTAACTCTCCCAGCCAACAAGAATGGTATTGCTCATTTGG
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173; Conserv
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On Jun 12, 2001 this sequence version replaced gi:13701842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,Cui,L., Oguchi,A., Aoki,K., Nagai,Y., Lian,J., Ito,T., Kanamori Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A., Mizutani-Ui,Y., Takahashi,N.K., Sawano,T., Inoue,R., Kaito,C., Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J., Kanehisa,M., Yamashita,A., Oshima,K., Furuya,K., Yoshimo,C., Shiba,T., Hattori,M., Ogasawara,N., Hayashi,H. and Hiramatsu,K. Whole genome sequencing of meticillin-resistant Staphylococcus
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and Kikuchi,H.
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AP003136.2 GI:14349228
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hypothetical protein
endopeptidase"
                                                                                                                                                                                                                                                    OGYTISKIKHAPQPEVNFKQFRTARHLTSVLAEVNDEDIGAMVIKLVKLIFMLDYVLFHSIQKSYTTHMELKNCFDYJAELDNHYALAWYRRTLECYTEPQIDDTNDGIVFSELTHESIQKSYTENASKFVVQFFHPLIADAVANDFSLSQNILLTGSMSGKSTFMKSIAINILLASAIQTVTSKFVQPGIVFTSNAANADDVLSGDSYFMAELKSIKRIVEIFDNQKIYCIDBIFKGTNTSKRIVAPSESVLSFLHEKSNFRVIAATHDIELAELLKQRYENYHFNEVIENNNIHFDYKIKPGKANTRNAIELLKITSFPAKIYERAKDNVSNG"
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aureus N315 genomic DNA,
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5292. .6980
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EDLNQPFIYIGKDTIKLQDELQGEVIAQLPNASVMYQLIDKPTDVHTFTPKYHKLAEA
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N-acetyltransfer"
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                                                                                                                                                                                                                                     635 AATATATTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACTACTATGTCGGATATAGTG 694
                                          GTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAATTTCCAATTTGTGTG 814
                                                                                                                                         ANAGTATGTGTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTG
                                                                                                                                                                                                                                                                                     173;
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8777. .9031
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VFCKEQQTIEKIGKITMGEAIVTTDVCGHOMAAAGPYPFKNHGOWVTSGGLGTMGFGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lafahgfnihfgviqppadvdvflvapkgpghlvrttfvegsavpslfgiqqdasgqa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="ORFID:SA1861"
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Pred. No. 15;
0; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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10882.960 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	_	_ •	_			4.3	0		Result	
41.2	41.6	7 41.6	41.6	41.6	41.6	42.2	2 43	43.8	!	
3.9	3.9	3.9	3.9	3.9	3.9	4.0	4.0	4.1	Query Score Match	
7491	82689	81905	40862	3024	3006	50000	3346	14041	Query Query Match Length DB	
21	24	24	24	24	24	24	18	22	Bd	
AAA70156	ABQ67198	ABQ69244	ABL34073	ABQ67866	ABQ69272	ABL56201	AAV74457	AAH48024	ID	
Plasmodium falcipa	Listeria innocua p	Listeria innocua D	Human immune syste	Listeria innocua D	Listeria innocua D	AmEPV genome fragm	Staphylococcus aur	Internal control B	Description	

Internal standards useful for nucleic acid amplification assays, comprises a synthetic nucleic acid made by non-recombinant techniques

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22222	122122222	22222112222 4444604444004	222222222	2222
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Human cnemically p Human immune syste Long terminal repe Human immune syste Human ovarian and	ĸ ₽	P 0 #	Human metastasis a porcine myostatin Human immune syste Tumour suppressor Human angiogenesis B. burgdorferi ant Tumour suppressor Yeast ADD9604-asso	Human chemically p Human immune syste Chemically treated Human immune syste

ALIGNMENTS

X P T T X R	K K K K	# X # X	X B X B	X S X X	XBX	3888	RESULT 1 AAH48024 ID AAH
WPI; 2001-408658/43. Internal standards useful for nucleic acid amp comprises a synthetic nucleic acid made by non	(BAXT) BAXTER AG. Zimmermann K, Turecek P, Schwarz H, Rieger	20-DEC-2000; 2000WO-EP12996. 22-DEC-1999; 99AT-0002170.	WO200146463-A2. 28-JUN-2001.	Internal control; ss. Parvovirus.	ternal control B19	AAH48024; 18-SEP-2001 (first entry)	LT 1 8024 AAH48024 standard; DNA; 14041 BP.

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RESULT 2
AAV74457/c
ID AAV744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods for the preparation and use of internal controls for nucleic acid amplification assays. The internal controls comprise a synthetic nucleic acid made by non-recombinant techniques. The internal controls are useful for detecting nucleic acids in a sample such as blood, spinal fluid, semen, saliva, tears, cell culture fluid, recombinant cells, animal tissue or plant tissue, by a quantitative PCR assay, by adding the internal control to the sample, amplifying the nucleic acids in the sample and detecting the amplified products. The internal controls help in performing the nucleic acid amplification assay quickly, and inexpensively without sacrificing assay specificity or sensitivity. The present sequence is one such internal control, which was used in an example to illustrate the present
    16-MAR-1999
                                            AAV74457;
                                                                                    AAV74457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14041 BP; 2151 A; 1354 C; 466 G;
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This sequence differs from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 CTAGTTCTTTCACAGTTTTCGGATTGTATCAACAATTACTCCAATCATCATCAGCTG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTTGATATCAAGGCCTCTGATCTTCCACAATCTGGTGACCAAGTCAACAAGGATATCA 583
                                                                                                                                                                                      RSTWRACTNSWRNHBTDNCSAMSANDANDTHTWTHRTSTSWRSTVNCNT
                                                                                                                                                                                                                          TGAGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAATTGTGCTGGTGT
                                                                                                                                                                                                                                                                    SMMNDSVSSAMSSTVWHRASNRHANDSTHCRSTASDSCRBDBYKAMTTADDNTWRKRMCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTTTGGACTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BYSMMNDSTAANDTTHHMNSTDCRASDSCRBDBYKAMTTAASAMSWRNDNDNTYTRACTD 11258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAATTCCAATTTGTGTGATGAAAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NASWRADDDTASMATHSAMWASTRACTDANDTHNSBCTDTCCRTTHNSTDCRASDSCRBD 11198
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                                                                                                                                                                                                                                                                                                              CAAACTTTTATGCTCAATTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTT 1003
                                                                                                                                                                                                                                                                                                                                                      ABTHCMARSNTHTHRMTHDSSHWSACMARABSNSTVTYANDSCCTYRMTHDANDTHMTHD
                                                                                                                                                                                                                                                                                                                                                                                          TGGGTCTCGGATTAACTCTCCCAGCCAACAAGAATGGTATTGCTCATTTGGCTAAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     ANDSBCTDTTHDRNTCRSNCDNGSTVANDNGATVCNTRTHRTMSTHRSTSARSMMARDNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANMRSTVSAMSARMATYCSTHNTRNACNTRTHWSTNMBRNCSSARYAWAYSADNGTCRSG 11138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCTGTAAAGCAAGGTAAACCAATTTCAAACTACTATGTCGGATATAGTGAAAGTATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARANATNRTHSRGNTTVWASCTDANDTHRRCMARDDRNTSCNSSTNGTHASMADNRSTBT 11078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAAAAATATAGAACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATATTA
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                                                                                    standard; DNA; 3346
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Pred. No. 0
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Rosen Barash SC,

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Kunsch

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GENOME

SCI INC Dillon

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skin infection; surgical toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus
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05-JAN-1996;
                                            07-JAN-1997;
                                                                                                                                        EP786519-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellulitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer readable medium; vaccine;
                                                                                           30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adable medium; vaccine; S.aureus infection; immunodetection;
eyelid infection; food poisoning; osteomyelitis; therapy;
ion; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                          given in the
2761..2820
/*tag= b
/note= "these bases r
96US-0009861.
                                               97EP-0100117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus
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                                                                                                                                                                                                                                                                                                                                                                                                          /note=
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are included
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                                                                                                                                                                                                           represent a line of missing text in elisting in the specification. They to maintain the nucleotide numbering
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                                                                                                                                                                                       DNA sequence"
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Polynucleotide(s) and proteins derived from stored on computer readable medium and used Claim 1; Page 754-756; 3271pp; on computer readable English. Staphylococcus aureus in the production of

This sequence represents one of 5191 Staphylococcus aureus DNA sequences confit the invention. The DNA sequences are recorded on a computer readable confidum, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so condustrial importance can be obtained. Specifically, sequences which are collikely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CS.aureus in a sample. S.aureus is implicated in numerous human diseases, cincluding cellulitis, eyelid infections, food poisoning, osteomyelitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer readable medium.

Sequence 3346 BP; 1086 A; 437 C; 556 G; 1143 T; 124 other;

Ś Matches Query Match Best Local S 139; Similarity Conservative 40.8%; 0 Pred. No. 0.60 0; Mismatches Score 43; N O DB 18; . 66; 200; Length 3346; Indels 2; Gaps

В 2915 430 TATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAGTTTTCGGATTG 489 TTTAATAAAATTCCACATCTCAATTTCACCTCTGTTAAATTAAATACCTATCTACATTTC

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RESULT 3
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                        invention are useful for delivering a polynucleotide encoding a protein to a vertebrate cell preferably a mammalian cell, such as a human cell. The vector is introduced into the vertebrate cell by infection in a viral particle, or by transfection, transduction, or injection either in vitro or in vivo. The vector is useful for the delivery and expression of biologically useful proteins in gene therapy protocols, and for delivering large DNA segments for engineering of vertebrate cells. Polynucleotides of the invention have applications in techniques such as their use as insertion sites for foreign genes of interest, hybridisation probes for charges and sites for foreign genes of interest, hybridisation
                                                                                                                                                                                                                                                                                           The invention relates to a recombinant entomopox virus (EPV) vector, comprising a polynucleotide encoding a protein operably linked with a heterologous promoter sequence. The invention also concerns methods for providing gene therapy for genetic deficiency disorders. Vectors of the invention are useful for delivering a polynucleotide encoding a protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant entomopox virus vector useful for delivering polynuclectide encoding protein to vertebrate cell, comprises polynuclectide encoding protein operably linked with heterologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 175-201; 326pp; English.
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14-SEP-2000; 2000US-0662254.
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      for chromosome
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and gene mapping,
   in PCR technologies,
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                                                                                                          (INSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of sense or antisense nucleic acids. Vectors of the invention provide for stable integration and expression of heterologous DNA in host cells, and are adapted for accepting large heterologous polynucleotide inserts which can be delivered in an infected or transformed cell and expressed in a stable fraction. The current sequence represents a framework of the genome of the genus B entomopoxvirus from amsacta moorei
                     New genomic sequences from Listeria species, useful for detection treatment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                                         Antibacterial; infection; ds.
                                                                                                                                               04-OCT-2000;
                                                                                                                                                                        04-OCT-2001; 2001WO-FR03061
                                                                                                                                                                                                                                                 Listeria innocua
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                                                                                  Glaser P;
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                                                                                                           PASTEUR.
                                                                                                                                               2000FR-0012697
                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                    Listeria; food contamination; mutational analysis;
                                                                                                            NAT
                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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46.2%;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                             #711.
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be
                          New genomic sequences from Listeria species, useful treatment and prevention of infection, also related antibodies and modulators -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present inventi
(ABQ67188-ABQ71212)
Claim 7; SEQ ID 679; 180pp; French
                                                                                    WPI; 2002-332479/37.
                                                                                                             Kunst F,
                                                                                                                                                                                   04-OCT-2000; 2000FR-0012697.
                                                                                                                                                                                                               04-OCT-2001; 2001WO-FR03061.
                                                                                                                                                                                                                                           11-APR-2002
                                                                                                                                                                                                                                                                     WO200228891-A2
                                                                                                                                                                                                                                                                                                Listeria innocua
                                                                                                                                                                                                                                                                                                                            infection;
                                                                                                                                                                                                                                                                                                                                          Antibacterial; Listeria; food contamination; mutational analysis;
                                                                                                                                                                                                                                                                                                                                                                     Listeria innocua DNA sequence #668.
                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ67866 standard; DNA; 3024
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                                                                                                               Glaser P;
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                                                                                                                                           CENT
                                                                                                                                                      PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Pred. No. 1
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                                       for detection, polypeptides,
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RESULT 6
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                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and pathogenicity of Listeria (potential therapeutic agents), treating infections by Listeria, and are useful as immunogens
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                                                                                                                                                                                                                                                                           gene;
                                                                                                                                                                                                                                                                                                                                                                                                                Human immune
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            WPI; 2002-130909/17
                                          Olek A,
                                                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                 02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                  03-JAN-2002
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                                                                          (EPIG-)
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                                                                          EPIGENOMICS
                                          Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                     2000DE-1032529
2000DE-1043826
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                                                                                    New genomic sequences from Listeria species, useful treatment and prevention of infection, also related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria innocua
   Claim 5;
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SEQ ID 2057; 180pp; French.
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                                                                                    for detection, polypeptides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-Listeria vaccines.

Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic fo
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                     New genomic sequences from Listeria species, treatment and prevention of infection, also I
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                                          antibodies and modulators
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                                                                                                                                                            (CNRS
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Pred. No. 4.2;
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                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum; chromosome 2; antimalarial; malaria; protozoacide;
 Disclosure;
                              diagnosis
                                           Proteins encoded by chromosome Plasmodium falciparum, useful a
                                                                                        WPI; 2000-365347/31
                                                                                                                                                                                                                                                 05-NOV-1999;
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                                                                                                                                              ) HOFFMAN S.
) CARUCCI D.
) GARDNER M.
) VENTER J C.
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                              of P.falciparum
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Page 496-497; 577pp; English
                                                                                                                   Carucci
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Pred. No. 4.2;
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                                           of the human malarial parasite, antimalarial vaccines and in the
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 289
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                                                                                                                                                                                                                                                                                                                                                                                 vaccine
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(I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our underestanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by chromosome 2 of the human malarial parasite, Plasmodium falciparum Also described are: (1) nucleotide sequences (11) encoding (1); and vaccines against p. falciparum infection comprising (1) or (II). (1) and (II) are useful for the development of vaccines against p. falciparum infection. (1) and polyvolonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (1), are useful in the detection of infection with p. falciparum. Furthermore, useful in the detection of infection with p. falciparum.
                                                                                                                            vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
                                                                specifically mentioned within the specification.
                                                                                           protein sequences given in the present invention, but which are not
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Matches
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Best Local Similarity
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673
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                                                           AAAAGAATGATGATATAAAATTAATATAAAACTACATAATAATACAAGAAAATTGTCC
                                                                                       AAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTTTGGAC
                                                                                                                     TCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAATTCCAATTTGTGTGATGAA
                                                                                                                                                                               AAGGTAAAAAAAGAAATAGAAGGAATTAAGGAAAATATGAATATTAGACATAATAAT
                                                                                                                                                                                                           ATGTGTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTGGTACC 759
                                                                                                                                                                                                                                          ATATTTTATATGAATAAATATTTTTAATATATACTATTATATGTTTGATTATACAAAA
                                                                                                                                                                                                                                                                     ATTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACTACTATGTCGGATATAGTGAAAGT 699
                                                                                                                                                                                                                                                                                                    ATTTATGATAAAATAAAGAAACTTTTTTGAAAACCTTTTTTGAAAATTTTTTGGGATAAT 432
                                                                                                                                                                                                                                                                                                                                 ATCACTCAAAAATATAGAACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATAT 639
                                                                                                                                                                                                                                                                                                                                                                139;
674
                             881
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Pred. No. 2.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                163;
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ABK40092 standard; DNA; 9728

Human chemically pretreated

gene sequence #87 strand

21-MAY-2002

(first entry)

WO200202806-A2 Homo sapiens Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

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Sequence 7491 BP; 3252 A; 787 C; 964 G;

2488 T; 0 other;

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid comprising a sequence at composition of genes associated with pharmacogenomics according to one of the ceguences of the genes ALDHG (NM 000693), CYP11A (NM 000711), CYP11B1 (CC (NM 000497), CYP3A3 (NM 000776 and NM 017460), DPYD (NM 000110), EPHX2 (NM 001979), OCLN (NM 002538), TXNRDI (NM 003330), UGT8 (NM 000796, NM 01990), NM 019901, NM 019902, NM 019862, NM 019898, CC (NM 01989) and their complementary sequences, or a sequence (SI) chosen (CC from 87 sequences and their complements. The chemical pretreatment co convert cytosines (but not methyl-cytosines) in the convert cytosines (but not methyl-cytosines) (CC into uracils. Also included are an oligomer (II) in particular an CC cligonuclectide or a peptide nucleic acid (PNA) oligomer, comprising in CC each case at least one base sequence having a length of 9 nucleotides (CC which hybridises to or is identical to a chemically pretreated DNA of (CC genes associated with pharmacogenomics and their complements, arranged in CC each case at least one base associated with remethylation state (CGG) and/or detecting SNPs (single nucleotide polymorphisms) (CC fice set of 87 nucleic acids and their complements is useful for diagnosis coff the 87 sequences. The oligomers may also be used as PCR primers. (CC represents one the 87 DNA sequences or its complement. CC Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                     ches
                                                                                                                                                                                                   8737
                                                                                                                                                                                                                                                     8677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer -
                                                 8917 T 8917
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                          635 AATATATTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACTACTATGTCGGATATAGTG 694
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                  GAATGTATAATATGTGAGATGTATATTTTGAAG
                                                                                                                                                                         GTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAATTCCAATTTGTGTG
                                                                                                                                                                                                  AAGGTTTAATTAGGAAAAAAGAGATAATTATATAGTATTTTAGTATAGTATATTTATAG
                                                                                                                                                                                                                           AAAGTATGTGTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTG
                                                                                                                                                                                                                                                  GTAGTAGTAATAAGATAGTAGGTTATTATTATTATATATATATATATATGAGTGATTTTGATT
                                                                                                                       ATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATACTTTAGTTT
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                                                                                                                                                                                                                                                                                                                                                      9728
                                                                                                                                                                                                                                                                                                                                                                               .int/pub/published
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                                                                                                                                                                                                                                                                                                     Conservative
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2000DE-1043826
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Pred. No. 3;
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                                                                                                                                                            695
                                                                                                          755
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fraction diagnosis and treatment cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                                              635 AATATATTAACTCTGTAAAGCAAGGTAAACCAATTTCAAACTACTACTGTCGGATATAGTG 694
atgaaaagcaaaaggttgctgttgaagttatcaagaatttattgactaatactttagttt
                                                                                                   GTACCTCTGATAAGCCATACGTTTATACTGATGTTTTGGCTTTGAATTCCAATTTGTGTG
                                                                                                                                                                                                       AAGGTTTAATTAGGAAAAAAGAGATAATTATATATATTTTAGTATATATATATTTTATAG 8796
                                                                                                                                                                                                                                                          ANAGTATGTGTGAAATTAAGGATATCATCAGAGATCAACAATACAATGTTCAACTCATTG 754
                                                                                                                                                                                                                                                                                                             immune
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2972 A; 124 C; 1890 G; 4742 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment of chemically modified gene, useful nent of diseases associated with abnormal
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Pred. No.
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ABL70607/c
                                                                                                                                                                                                                                                      SSSSSSS
                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated With cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is CC to provide the chemically modified DNA of genes associated with cell csignalling, as well as oligonucleotides and/or PNA-oligomers for CC detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and compression of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL70111-ABL70626 represent chemically pre-treated CC genomic DNA's of genes associated with cell signalling.

CC Note: The sequence data for this patent is not represented in the printed CC Special Patent Office.
                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                        Matches
                                                                                                                            2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genom sequences of genes associated with cell signalling -
2510
                                                              2570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                European
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                               539
                                                                                             479
                                                                                                                                                       419 AAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAG 478
                                                                                                                                                                                                       Local
                                                                                                                          AAAAACCCTTTAAATTAAAAAATTTAATCTCTTAATAAAAACCAATTACAATACATAAACCA 2571
ATCCCCATCTTTAAAATTACATATTAÄÄATATTTÄCAAATÄATÄCAATÄTÄÄTÄT----
                           CCTCTGATCTTCCACAATCTGGTGACCAAGTCAACAAGGATATCACTCAAAAATATAGAA
                                                              TTTTCGGATTGTATCAACAATTACTCCAATCATCATCATCAGCTGCAGTTGATATCAAGG
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                                                                                                                                                                                                                                                                                  Patent Office.
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 497;
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                                                                                                                                                                                      Score 41; DB 2
Pred. No. 3.5;
0; Mismatches
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419 AAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAG 478

Matches Query Match Best Local S

158;

Conservative

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Pred. No. 3.5; 0; Mismatches Score 41; Pred. No.

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Length 15518;

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Gaps

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Similarity

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 RESULT 13
                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADLS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimez's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
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                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
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 Sequence 15518
                                                                                                                                                 Claim 1; SEQ ID NO 2145; 32pp + Sequence Listing;
                                                                                                                                                                            cytosine
                                                                                                                                                                                                                                   WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL34172;
                                                                                                                                                                                                                                                                                      (EPIG-)
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2000DE-1043826
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 7926 T;
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  other;
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RESULT 14
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PR 01-SEP
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CC genes
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Matches 158
                                                                                                 The present genes which
                                                                                                                                                               New nucleic acid derived useful for diagnosis of also for treatment -
                                                                                                                                                                                                                                                                                      06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metastasis associated gene; cytostatic; gene therapy; cancer; cytosine methylation; gene; ds.
                                                                                      used in
                                                                                                                                       Claim 1;
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                                                                        resent invention provides a number of human metastasis associated which are modified by cytosine methylation. The sequences can be in the diagnosis and treatment of cancer. The present sequence is f the genes of the invention.
  al Similarity
158; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis
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                                                  15518 BP;
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Pred. No. 3
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                                                                                                                                     Sequence Listing;
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Mismatches
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419 AAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTCACAG 478

The present sequence was used for comparison studies with a myostatin gene promoter sequence isolated from Mus musculus. Regulating the transcription activities or expression of the isolated promoter is usef for treating muscle associated disorders such as cancer, muscular dystrophy, spinal cord injury, neurodegenerative disorders, traumatic injury, congestive obstructive pulmonary disease (COPD), amylotrophic lateral sclerosis, acquired immunodeficiency syndrome (AIDS), cachexia or ageing. The promoter is useful for modulating the expression of the myosin gene for producing animal food products having increased muscle and protein content and reduced fat and cholesterol content, for

is useful

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ARESULT 15
ARP5862/G
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AC ARP586
AC A
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                                                                                                                                                                                                                                                                                                                                                                                               Novel myostatin gene promoter for regulating expression of heterologous genes in cells or animals, for identifying compounds that inhibit its activity or expression, which are useful for treating muscle disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porcine; pig; myostatin; promoter; cytostatic; anti-HTV; neuroprotective; immunomodulator; cancer; muscular dystrophy; spinal cord injury; neurodegenerative disorder; congestive obstructive pulmonary disease; COPD; amylotrophic lateral sclerosis; acquired immunodeficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2404
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                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12-13;
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Search completed: January 27, 2003, 04:31:07 Job time: 467 secs
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Best Local Similarity 49.1%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulating expression of a heterologous gene in cells or animals, to engineer host cells, to screen for compounds that inactivate or inhibit its transcription and expression, for inhibiting its expression in cells for the promotion of muscle growth, for diagnostic evaluation, genetic testing and prognosis of a disease or disorder associated with myostatin
                                                                                                                                                                                                                                                                                                                           1224 TGAAACTTTAAAATTGTAATTTAAATAAGTAATTCTTTTACACTTCATACTTAAAAAGTT 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                   1284 AATTAAAATCTATGTTAACAATAATATAAACTGCACTTAAATATTATTAATCTTTATTAG 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1537 BP; 519 A; 259 C; 236 G; 523 T; 0 other;
                                                                                                        1104 GAAAAAAGAATTTTATTTGCTGTTTTAAATTATTTTTAGT 1065
                                                                                                                                                                                                                1164 GAPATGTCTTTTTCCTCAAAAAAAATAAATGATTTTACATTATTTAGACAAACATTTGAG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression.
                                                                                                                                    979 GCCAAGGAAAGTGAAGTTAGAGTTTTTGAGATGTGTTGACT 1018
                                                                                                                                                                                                                                               919 GGTATTGCTCATTTGGCTAAATCATCAAACTTTTATGCTCAATTGAGCCAACAATTCGAT 978
                                                                                                                                                                                                                                                                                                                                                                             859 ACTAATACTTTAGTTTTGGACTTGTTGGGTCTCGGATTAACTCTCCCAGCCAACAAGAAT 918
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Result
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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*

5. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd
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          US-08-232-463-14
US-08-232-619-1
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PCT-US95-04075-1
US-08-553-633A-4
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US-08-913-159-9
US-09-134-001C-1569
US-09-148-970B-132
US-09-186-402B-7
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Sequence 1569, App
Sequence 166, Appli
Sequence 166, Appli
Sequence 132, Appli
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Sequence 19, Appl	Sequence 19, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 1263, Ap	Sequence 35, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US/07/935,313 FILING DATE: APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELEPHONE: (703)836-9300 TELEX: 899149 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid , CLUNE: pTZgpt-F18 US-08-232-463-14 RESULT 1 US-08-232-463-14 Sequence 14, Application US/08232463 PATERIX NO. 5670367 GENERAL INFORMATION: APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52 IMMEDIATE SOURCE: CLONE: pTZgpt-CORRESPONDENCE ADDRESS: TOPOLOGY: STRANDEDNESS: single STATE: VA CITY: Alexandria ADDRESSEE: E: Foley & Lardner 1800 Diagonal Road, linear Suite 500 #1.25

Query Match

5.18;

Score 54.2;

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Length 7218;

14.5%;

Pred. No.

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Matches 8
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                      APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin:
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
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                                                                                                                                                                                                    STREET: 1840 Dehavid
              CLASSIFICATION:
                                 FILING DATE:
                                                                                                                                                                         COUNTRY:
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83; Conservative
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                                                                                                                                                                                           California
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1840 DeHavilland
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/08221767
Patent No. 6268212
GENERAL INFORMATION:
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Best Local
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                         CLASSIFICATION: 800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 2287 base pair
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APPLICANT:
APPLICANT:
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LENGTH: 2287 base pairs
TYPE: nucleic acid
                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lichenstein, Henri S.
APPLICANT: Lyons, David E.
TITLE OF INVENTION: Tissue Specific Transgene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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LOCATION:
                                                                                                                                                                                                                                                STREET: 1840 Dehavilland CITY: Thousand Oaks STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: unknown
              TYPE:
                                                                                         FILING DATE:
                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                   COUNTRY:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                    91320-1789
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              nucleic acid
                           2287 base pairs
                                                                                                                                                                                                                                   USA
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                                                                                                                                         Version #1.25
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RESULT 4
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GENERAL INFORMATION:
APPLICANT: AMGEN
                                                                                                CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2287 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                             ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
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NAME/KEY:
                                      FEATURE:
                                                      MOLECULE TYPE:
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 NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                      STRANDEDNESS:
TOPOLOGY: unl
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/04075 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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318..2117
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318..380
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381..2114
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Pred. No. 0.32;
                                                                                                                                                                                                                                               Version
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RESULT 5
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Best Local Similarity
Matches 117; Conserv
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TELEFAX: (703)-205-805
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                       APPLICATION NUMBER: US/08/553,633A FILING.DATE: 01-APR-1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: BIRCH, ST
STREET: PO BOX 747
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                                                                  NAME: .SVENSSON, LEONARD R
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22040-0747
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                                                   TELEPHONE:
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HOLDEN, MATTHEW COX, ANTHONY RJ
                                     (703) -205-8050
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MCGOWAN, SIMON J
VENTION: PROCESS FOR ACTIVATING GENE EXPRESSION
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381..2114
                                                     (703) -205-8000
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Pred. No. 0.32;
                                                                                          009-104
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APPLICANT: Gil H.
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ORIGINAL SOURCE:
                                                                                                                                                                                                                          OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: En:
NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genu
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                        NAME: A. Anders Brookes
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key
CITY: Rockville
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                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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43.6%;
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US-08-487-826B-13
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APPLICANT: Sim, Ki
APPLICANT: Chitnis
APPLICANT: Miller,
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Best Local Sim
Matches 72;
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Sequence 13, App...
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                                                                                                              TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UNMERE: US/08/487,826
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pair
         MOLECULE NO
                                   TOPOLOGY: li
                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                  TYPE: nucleic
STRANDEDNESS:
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STRANDEDNESS: double
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T: 620 Newport Center Drive 16th
Newport Beach
California
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                                                                                  nucleic acid
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Miller, Louis H.
Peterson, David S.
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     16th Floor
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LENGTH: 825
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Best Local 9
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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RGANISM: Staphylococcus epidermidis
9-134-001C-1569
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AGATGTGTTGACTTTGCTAACAAGGAAGTTAAGAATTGT 1044
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                                                     AAAAGAGGTGCTTCAGATACATTTATAGTTGTTGATATGCCTATAGGGACTGTTGGTTTA
                                                                                      AACTTTTATGCTCAATTGAGCCAACAATTCGATGCCAAGGAAAGTGAAGTTAGAGTTTTG 1005
                                                                                                                          GGATATGATAGTACTGTTCAAGTTACATTGAACGATATGATTCATCATCATGGTAAGGCTGTT 216
                                                                                                                                                           GGTCTCGGATTAACTCTCCCAGCCAACAAGAATGGTATTGCTCATTTGGCTAAATCATCA
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Pred. No. 2
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Pred. No. 3.9;
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                                                                                                                                                                                                                                                                                                                                           Mismatches 152;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3706 base pair
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNIMBER: DK 0179/95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                1141
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                               610 TCAACAGTTGTTGCCTCTCAAAGAGAATATATTAACTCTGTAAAGCAAGGTAAACCAATT 669
                                                                                                                                                                                                                                                                                                                 OTHER
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IDENTIFICATION METHOD: experimen
OTHER INFORMATION: /codon_starte
OTHER INFORMATION: /product= "L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid sTRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                   OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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OTHER INFORMATION: /pi

OTHER INFORMATION: /pi
CAACAATACAATGTTCAACTCATTGGTACCTCTGATAAGCCATACGTTTATACTGA 785
                               GTTAATAATGATAAAGAATATTTCGTGAAAAAGTATAATGACACCTTTTCTCATAGAG
                                                              TCAAACTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGATATCATCAGAGAT 729
                                                                                              TCTACTGGTATTGCTACTCAAAAAGATAAACTTTATTTAATAGACTATACTAAAAAAAGAA 1142
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                                                                                                                                                                                                                                                 /standard_name= "Gene coding
endonuclease"
/label= r-llaBI
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/label= m-llaBI
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/product= "LlaBI methylase"
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/gene= "ORF"
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Pred. No. 5.3;
O; Mismatches
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US-09-484-970B-132/c
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; Sequence 166, Appl
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Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick F
                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 166:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
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                                                                                                                                      TTCTAGTT 469
                                                                                                      TTTCAGTT 36
                                                                                                                                                                       CTATTAACAATCCGGTGCTGAGATCTATTACCAATGAAATGATTCTCCTGCAGTATAATC
                                                                                                                                                                                                     CCTTTTAGAATTGGCTCAAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTC 461
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STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 16950
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Plunkett, on
Plunkett, on
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Porma, Nicole T.
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Pred. No. 8.7;
0; Mismatches 58;
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LENGTH: 1766
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Best Local Similarity
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                                                                                     INFORMATION FOR SEQ ID NO:
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                    FILING DATE: 02-SEP-
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Wi
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 660 Whit
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Gateway 2000 OPERATING SYSTEM: DOS
                                                                                                                   TELEFAX:
                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                    STRANDEDNESS:
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                                                  LENGTH:
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                 nucleic acid
DEDNESS: single
                                                                                                                                                                                                      Kurt G. Briscoe
                                                2728 base pairs
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                                                                                                                    (914) 332-1844
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Sequence 7, Application US/08836402B Patent No. 6063988
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CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 245065.1CB1
REFERENCE/DOCKET NUMBER: BETELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700
                                                                                                        FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rudiger Hain, Regina Fischer TITLE OF INVENTION: DNA SEQUENCE AND ITS USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609 TTCAACAGTTGTTGCCTCTCAAAGAGAATATATTAACTCTGTAAAGCAAGGTAAACCAAT 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     660 White Plains Road
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                                                                                                                                                         44 40 200.7 (Germany)
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                                                            33,141
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                                              Bayer 9840-KGB
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Pred. No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION 435
PRIOR APPLICATION NUMBER: 07/881,054
APPLICATION NUMBER: 07/278,735
APPLICATION NUMBER: 07/278,735
FILING DATE: 2-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
NAME: CHARLES A. MUSERLIAN
19.683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DUWAS, BRUNO; GERVAIS, MONICA;
APPLICANT: DERGION, MAX; JOURDAN, MIREITTE; JOUSSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-195-814-1/c
                                                                                                                                                                                                           TELEFAX: (212) 661-8002
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5910
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 14-FEB-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BERGION, MAX; JOURDAN, I
APPLICANT: FRANCOISE XAVIERE
TITLE OF INVENTION: NOVEL PLASMIDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1319 TCAAGCATTTCTTCGGTCAAATGAATGTAACGCTTCTTGATCATTGATTTGTCACCTGTA 1260
                                                                    ORIGINAL SOURCE
                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.1029-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: LARVAE
                                                                                                                        TOPOLOGY:
                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: UNKNO
                                                                                                                                                                                                                                            TELEPHONE:
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                                                  ORGANISM:
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                              DENSOVIRUS OF JUNONIA
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milarity 50.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5262158
GENERAL INFORMATION:
APPLICANT: Payne,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO:
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LOCATION: 1
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURREST APPLICATION DATA:
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                                         REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S
TELECOMMUNICATION INFORMATION:
                                                                          CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
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CELL TYPE: S
CELL LINE:
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                               TELEPHONE:
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OTHER INFORMATION:
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2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                            USA
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                               904-375-8100
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6.9;
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O 50 NUCLEOTIDES IN LENGTH
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SEQUENCE CHARACTERISTICS:

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; IMMEDIATE SOURCE:
; CLOUR: E. COli NM522 (pMYC2320) NRRL B-18769
US-07-876-280-29
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                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, Roman
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3471 base pairs
TYPE: NUCLEIC ACID
STEAMATENNESS: 40:011
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Best Local Similarity 55.4
Matches 67; Conservative
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Versi
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
CCLASSIFICATION: 435
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HYPOTHETICAL: N
ANTI-SENSE: NO
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STRANDEDNESS: down
TOPOLOGY: 1'
OLECULP'
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ORGANISM: Bacillus the
STRAIN: kumamotoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Foncerrada, Lui
APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
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ADDRESSEE: Roman Saliwanchik
STREET: 2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding
TITLE OF INVENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 2
HYPOTHETICAL:
                 TOPOLOGY: 1:
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STATE: F:
COUNTRY:
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                                                   STRANDEDNESS:
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                                     linear
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No
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               DNA (genomic)
                                                       double
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55.4%;
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Pred. No. 7.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                         Version
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; LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF LUIS
; LIBRARY: FONCERRADA
; CLONE: 50C
US-07-812-180A-1
Search completed: January 27, 2003, 05:36:48 Job time : 114 secs
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Best Local Similarity 55.4%;
Matches 67; Conservative
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ORIGINAL SOURCE:
ORGANISM: Bacillus thur
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS5
IMMEDIATE SOURCE:
                                                                                                                                                                                                            491 CTAGAAGTGTTGTTTCTAATCAATTTATAGCTTTAGATCTTAACTTTGTTAGTTCAATTC 550
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Pred. No. 7
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0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^{\prime}number of hits satisfying chosen parameters:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                   Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

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9: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

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11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        January 27, 2003, 05:30:37; Search time 58 Seconds (without alignments) 8272.669 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396772 seqs, 224632407 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd
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2550	543	371	371	2295	2295	116592	2000	1503841	1503841	1503841	31517	536	490	2282	2280	392	491	Match Length
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US-09-764-864-318	US-09-764-847-471	US-09-796-692-5606	US-09-796-692-2970	US-09-815-242-6496	US-09-815-242-3894	US-09-818-512-3	US-09-938-842A-4858) US-09-795-686-1) US-09-795-668-1	US-09-946-807-1	US-09-070-927A-180	US-09-834-975-317	US-09-783-590-6019	US-09-880-107-2192	US-10-044-090-450	US-09-960-352-11703	US-09-878-574-4301	ID
Sequence 318, App	Sequence 471, App	Sequence 5606, Ap	Sequence 2970, Ap	Sequence 6496, Ap	Sequence 3894, Ap	Sequence 3, Appli	Sequence 4858, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 180, App	Sequence 317, App	Sequence 6019, Ap	Sequence 2192, Ap	Sequence 450, App	Sequence 11703, A	Sequence 4301, Ap	Description
	10 US-09-764-864-318 Sequence	10 US-09-764-847-471 Sequence	16 35.2 3.3 371 9 US-09-796-692-5606 Sequence 17 35.2 3.3 543 10 US-09-764-847-471 Sequence 18 35.2 3.3 2550 10 US-09-764-864-318 Sequence	15 35.2 3.3 371 9 US-09-796-692-2970 Sequence 16 35.2 3.3 371 9 US-09-796-692-5606 Sequence 17 35.2 3.3 543 10 US-09-764-847-471 Sequence 18 35.2 3.3 2550 10 US-09-764-864-318 Sequence	14 35.6 3.3 2295 10 US-09-815-242-6496 15 35.2 3.3 371 9 US-09-796-692-2970 S 16 35.2 3.3 371 9 US-09-796-692-5606 S 17 35.2 3.3 543 10 US-09-764-847-471 18 35.2 3.3 2550 10 US-09-764-864-318	13 35.6 3.3 2295 10 US-09-815-242-3894 14 35.6 3.3 2295 10 US-09-815-242-6496 15 35.2 3.3 371 9 US-09-796-692-2970 S 16 35.2 3.3 371 9 US-09-796-692-6066 S 17 35.2 3.3 371 9 US-09-764-847-471 18 35.2 3.3 2550 10 US-09-764-864-318	12 35.8 3.4 116592 10 US-09-818-512-3 13 35.6 3.3 2295 10 US-09-815-242-3894 14 35.6 3.3 2295 10 US-09-815-242-6496 15 35.2 3.3 371 9 US-09-796-592-2970 S 16 35.2 3.3 371 9 US-09-796-592-5666 S 17 35.2 3.3 543 10 US-09-764-847-471 18 35.2 3.3 2550 10 US-09-764-864-318	11 35.8 3.4 2000 9 US-09-938-842A-858 S 12 35.8 3.4 116592 10 US-09-818-512-3 13 35.6 3.3 2295 10 US-09-815-242-3894 14 35.6 3.3 2295 10 US-09-815-242-6496 15 35.2 3.3 371 9 US-09-796-692-2970 16 35.2 3.3 371 9 US-09-796-692-5606 17 35.2 3.3 371 9 US-09-764-847-471 18 35.2 3.3 250 10 US-09-764-864-318	10 36.6 3.4 1503841 10 US-09-795-686-1 11 35.8 3.4 116592 10 US-09-918-512-3 13 35.6 3.3 2295 10 US-09-815-242-3894 S 14 35.6 3.3 2295 10 US-09-815-242-6496 S 15 35.2 3.3 371 9 US-09-796-692-5970 Se 16 35.2 3.3 371 9 US-09-796-692-5606 Se 17 35.2 3.3 371 9 US-09-764-847-471 S 18 35.2 3.3 2550 10 US-09-764-864-318 S	9 36.6 3.4 1503841 10 US-09-795-6668-1 10 36.6 3.4 1503841 10 US-09-795-686-1 11 35.8 3.4 2000 9 US-09-938-942A-4858 12 35.8 3.4 16592 10 US-09-818-512-3 13 35.6 3.3 2295 10 US-09-815-242-3894 14 35.6 3.3 2295 10 US-09-815-242-6496 15 35.2 3.3 371 9 US-09-796-692-2970 16 35.2 3.3 371 9 US-09-796-692-2970 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US-09-764-847-471 S 35.2 3.3 2550 10 US-09-764-864-318 S	6 37.6 3.5 536 10 US-09-834-975-317 S 7 37.2 3.5 31517 10 US-09-070-927A-180 S 8 36.6 3.4 1503841 9 US-09-946-807-1 S 9 36.6 3.4 1503841 10 US-09-795-668-1 S 10 36.6 3.4 1503841 10 US-09-795-686-1 S 11 35.8 3.4 12000 9 US-09-938-842A-4858 Se 12 35.8 3.4 116592 10 US-09-818-242-3894 S 13 35.6 3.3 2295 10 US-09-818-242-3894 S 14 35.6 3.3 2295 10 US-09-818-242-6496 S 15 35.2 3.3 371 9 US-09-786-692-2970 Se 16 35.2 3.3 371 9 US-09-786-892-6976 Se 17 35.2 3.3 371 9 US-09-786-892-6976 Se 18 35.2 3.3 371 9 US-09-786-892-6976 Se 18 35.2 3.3 371 9 US-09-786-892-6976 Se 19 35.2 3.3 371 9 US-09-786-892-6976 Se 10 35.2 3.3 371 9 US-09-786-892-6976 Se	5 38.2 3.6 490 10 US-09-783-590-6019 S 6 37.6 3.5 536 10 US-09-970-927A-180 S 7 37.2 3.5 31517 10 US-09-970-927A-180 S 8 36.6 3.4 1503841 9 US-09-946-807-1 S 9 36.6 3.4 1503841 10 US-09-795-668-1 10 36.6 3.4 1503841 10 US-09-795-668-1 11 35.8 3.4 2000 9 US-09-938-842A-4858 S 11 35.8 3.4 12592 10 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US-09-970-927A-180 S 8 36.6 3.4 1503841 9 US-09-946-807-1 S 9 36.6 3.4 1503841 10 US-09-95-668-1 S 10 36.6 3.4 1503841 10 US-09-795-668-1 S 11 35.8 3.4 2000 9 US-09-98-842A-4858 Se 12 35.8 3.4 116592 10 US-09-818-242-3894 S 13 35.6 3.3 2295 10 US-09-818-242-3894 S 14 35.6 3.3 2295 10 US-09-818-242-6496 S 15 35.2 3.3 371 9 US-09-786-692-2970 Se 16 35.2 3.3 371 9 US-09-786-892-6976 Se 17 35.2 3.3 371 9 US-09-786-892-6976 Se 18 35.2 3.3 371 9 US-09-786-892-6976 Se 18 35.2 3.3 371 9 US-09-786-892-6976 Se	2 40 3.7 392 10 US-09-960-352-11703 S 3 39.6 3.7 2280 12 US-10-040-900-450 S 4 39.6 3.7 2282 10 US-09-880-107-2192 S 5 38.2 3.6 490 10 US-09-783-590-6019 S 6 37.6 3.5 536 10 US-09-795-317 S 7 37.2 3.5 31517 10 US-09-946-807-1 S 9 36.6 3.4 1503841 9 US-09-946-807-1 S 10 36.6 3.4 1503841 10 US-09-795-668-1 US-09-995-668-1 S 11 35.8 3.4 1203841 10 US-09-795-688-1 S 12 35.8 3.4 116592 10 US-09-938-842A-4858 S 13 35.6 3.3 2295 10 US-09-815-242-3894 S 14 35.6 3.3 371 9 US-09-796-692-2970 S 15 35.2 3.3 371 9 US-09-796-692-2970 S 16 35.2 3.3 371 9 US-09-796-692-2970 S 17 35.2 3.3 371 9 US-09-796-892-9970 S 18 35.2 3.3 3250 10 US-09-796-892-6966 S 18 35.2 3.3 3250 10 US-09-796-892-6976 S 19 35.2 3.3 3250 10 US-09-796-892-6976 S 19 35.2 3.3 3250 10 US-09-796-892-6976 S 10 35.2 3.3 3250 10 US-09-796-894-318 S	1 42.4 4.0 491 10 US-09-878-574-4301 S 2 40 3.7 392 10 US-09-980-352-11703 S 3 39.6 3.7 2282 10 US-109-880-107-2192 S 4 39.6 3.7 2282 10 US-09-880-107-2192 S 5 38.2 3.6 490 10 US-09-783-590-6019 S 6 37.6 3.5 536 10 US-09-975-317 S 7 37.2 3.5 31517 10 US-09-946-807-1 S 9 36.6 3.4 1503841 9 US-09-946-807-1 S 10 36.6 3.4 1503841 10 US-09-995-668-1 US-09-995-688-1 S 11 35.8 3.4 1203841 10 US-09-995-688-1 S 12 35.8 3.4 116592 10 US-09-915-242-3894 S 13 35.6 3.3 2295 10 US-09-815-242-6496 S 15 35.2 3.3 371 9 US-09-796-692-2970 S 16 35.2 3.3 371 9 US-09-796-692-2970 S 17 35.2 3.3 371 9 US-09-796-692-2970 S 18 35.2 3.3 3250 10 US-09-764-847-471 S

ALIGNMENTS

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
APPLICANTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
FRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-878-574-4301
                                                                                                                                                                                                                                                                                           US-09-878-574-4301
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SEQ ID NO 4301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4301, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                 Matches 121;
                                                                                                                                                                                                                                                                                                    IENGTH: 491
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1) . (491)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-A11
 177
                                   238
                                                                     117
                                                                                                                                                                               118 GTTTCCGGATATAATATCGAATATACCGAATTTGATTGTTACAGTGATGCTAGTCTTCAA 177
                                                                                                                                           57
                                egrercaagaerrregargaarcarregrecererracregrearrrecaraerrr
                                                                                                         Conservative
                                                                                                                                                                                                                                  47.8%;
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                                                                                                                                                                                                                                  Score 42.4; DB 10;
Pred. No. 0.24;
                                                                                                                                                                                                                   Mismatches 132;
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                                                                                                                                                                                                                                                   Length 491;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                   Gaps
                                 297
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
ITITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TER OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT APPLICATION INVESTE AND FAT DEPOSITION
CURRENT APPLICATION UNMEBER US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11703
LENGTH: 392
TYPE: nw"
                                                                                                                                                                                                                                   US-10-044-090-450; Sequence 450, Application US/10044090; Patent No. US20020137081A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; OTHER INFORMATION: Clone ID: 50-LIB3058-031-Q1-K1-E6
US-09-960-352-11703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 49.1
Matches 106; Conservative
                                                                                      NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 450
LENGTH: 2280
                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                           APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/044,090 CURRENT FILING DATE: 2002-01-09
         FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Inc
                                                      ORGANISM: Homo sapiens
NAME/KEY: unsure
                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                        333
                                                                                                                                                                                                                                                                                                                                                                                                                  273
                                                                                                                                                                                                                                                                                                                                                                                                                                              234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTACTGGTGATTTGCATAGTTTTTGTTTCCTCAAGTGCCTCTGTCAATGGTTCCGTTTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTCCATATCTTTGTTTTCTTTGGGTGGTGTCAAGAGTTTTGGATGAATCATTGGTTCGTGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTTACAGTGATGCTAGTCTTCAAAGTCTTCCAGATGTTTTCTCAACTGATAGCATTTT 212
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                Incyte
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49.1%;
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                ID No.
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Pred. No. 0.87;
                US20020137081A1 351158.4
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; LOCATION: 1282
; OTHER INFORMATION: a,
US-10-044-090-450
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US-09-880-107-2192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
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SEQ ID NO 2192
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Best Local Similarity
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APPLICANT: Vockley, Jos
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic,
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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2282
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                  357
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                                         AAATTĆĆATĀĀĠTCTTŦATATTCĀGGCTACTCTTTATTTTTGAAAACTCATTTTCTATCA 235
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Pred. No. 2.1;
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TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2

RRENT APPLICATION NUMBER: US/09/783,590

CURRENT FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 08/420,856

PRIOR APPLICATION NUMBER: 08/346,731

PRIOR APPLICATION NUMBER: 08/346,731

PRIOR APPLICATION NUMBER: 08/346,731

PRIOR PRIOR DATE: 1994-11-21

NUMBER OF SEQ ID NOS: 12485

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6019

LENGTH: 490

TYPE: DN'
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (140)
OTHER INFORMATION: n equals a,t,g,
                             OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (299)
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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LOCATION: (58)
OTHER INFORMATION: n equals
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                          LOCATION: (285)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (294)
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OTHER INFORMATION: n equals a,t,
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ORGANISM: Homo sapiens
FEATURE:
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                                                                    LOCATION: (450)
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             OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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LOCATION: (431)
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OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature

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APPLICANT: Lilie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Wan Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TILE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREV
TILE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 317
LENGTH: 536
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                                                                        Query Match
Best Local 9
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LOCATION: (476)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (489)
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OTHER INFORMATION: n equals
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NAME/KON: misc_feature
LOCATION: (1)...(536)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                LENGTH: 536
TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: n equals
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LOCATION: (472)
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334 GGTTTCCCACAATACTTGTGCTCAAAACTTTTTATTGTCCTCAACAAATGGTACTCAACAA 393
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                                                       7 Match 3.5%;
Local Similarity 46.8%;
nes 94; Conservative
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les 70; Conserv
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                                                  Score 37.6; DB 10; Length 53
Pred. No. 3.8;
0; Mismatches 107; Indels
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US-09-070-927A-180/c
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Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                             Query Match
Best Local S
                                       24369
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 180
SEQUENCE CHARACTERISTICS:
                                                                          189
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249 TTTGGATGAATCATTGGTTCGTGGTGTTACTGGTGATTTGCATAGTTTTGTTTCCTCAAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION = CUNROWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                               Local Similarity hes 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 180:
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                                                                          TGTTTTCTCAACTGATAGCATTTTCCTTCCATATCTTGTTTCTTTTGGGTGGTGTCAAGAG 248
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                                                                                                                                                                                                                                               LENGTH: 31517 base pairs TYPE: nucleic acid STRANDEDNESS: double
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ilarity 55.4%;
Conservative
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Pred. No. 20;
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CURRENT APPLICATION NUMBER: US/09/946,807
RRENT FILING DATE: 2001-09-05
IOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/515,716
PRIOR APPLICATION NUMBER: US/09/515,716
PRIOR FILING DATE: 2000-02-8
PRIOR FILING DATE: 2000-02-8
NUMBER OF SEQ ID NOS: 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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Patent No. US20020165144A1
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
                                                LOCATION: (1)...(1531)
OTHER INFORMATION: v=a
                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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OTHER INFORMATION: d=a
                                                                                                                                                                                                                                                          LOCATION: (1)...(1531)
OTHER INFORMATION: b=g or c
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NAME/KEY: misc_feature
LOCATION: (1)...(1531)
                                                                                                                        OTHER INFORMATION: h=a
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LOCATION: (1)...(1531)
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OTHER INFORMATION: y=t/u
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LOCATION: (1)...(1531)
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OCATION: (1)...(1531)
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTMARE: FastSEQ for Windows Version 4.0
OTHER INFORMATION: v=a NAME/KEY: misc_feature LOCATION: (1)...(1531)
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: 8=g
NAME/KEY: misc feature
TOCATION: (1) (1531)
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NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
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OTHER INFORMATION: h=a
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OTHER INFORMATION: m=a
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Pred. No. 93;
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                                       NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: h=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
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ORGANISM: Homo sapiens
                                                                                                                                         LOCATION: (1)...(1531)
OTHER INFORMATION: d=a or
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OTHER INFORMATION: w=a or t/u
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LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
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OTHER INFORMATION: m=a
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INFORMATION: v=a
KEY: misc_feature
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Pred. No. 9
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RESULT 12
US-09-818-512-3
; Sequence 3, Application US/09818512
; Patent No. US20020142416A1
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SEQ ID NO 4858
LENGTH: 2000
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Best Local :
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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GENERAL INFORMATION:

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SOFTWARE: Fast
SEQ ID NO 3894
LENGTH: 2295
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SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
TYPE: DNA
ORGANISM: Human
FEATURE:
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                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
DBIOR APPLICATION NUMBER: 60/253,625
DBIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                         PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
                                                                     NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
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TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND
TITLE OF INVENTION: THEREOF
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LOCATION: (1)...(116592)
OTHER INFORMATION: n = A,T,C or
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PPLICANT: Xu, H. Howard
THLE OF INVENTION: Identification of
ITLE OF INVENTION: Prokaryotes
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t Local Similarity
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                                                                                                                                        APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
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                                            FastSEQ
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Trawick, John D.
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Pred. No. 70;
0; Mismatches
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US-09-815-242-6496/c
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/219,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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SEQ ID NO 6496
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith |
APPLICANT: Wall, Daniel
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PRIOR APPLICATION NUMBER: 60/269,308
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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LOCATION: (1)
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TTTGGATGAATCATTGGTTCGTGGTGTTACTGGTGATTTTGCATAGTTTTTGTTTCCTCAAG 308
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                                                             TÉGTTCTTCATCATGTAGTTTATCCTTTGTCTGTGGTTGTTCACTTTTGGCTTTTTCTGC 145
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Xu, H. Howard
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Trawick, John D.
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Pred. No. 20;
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Search completed: January 27, 2003, 07:48:41 Job time: 4938 secs
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CURRENT FILING DATE: 2001-03-01
LIOR APPLICATION NUMBER: 60/186,126
RIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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Best Local Similarity 50.6%;
Matches 85; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2970
LENGTH: 371
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
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PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
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MRGANISM: Homo sapiens
9-796-692-2970
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28
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APPLICATION NUMBER: 60/206,201
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is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail : CNS000D1 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR01J16 of RPCI-98 library from Drosophila melanogaster (fruit Direct Submission fly), genomic survey sequence. AL065414 Genoscope. AL065414.1 GI:4938827 National de Sequencage : segref@genoscope.cns.fr

Result

Score

Query Match

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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                      CAAAAGGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACA
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TCAAATATYMACATTYCCMCYATTWTTTAWYACYAAAYWTTYYCCTAAAATTTYYTTTTWW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Library constructed by N. Garrett, K. Ryan and A.M. Zorn
(Wellcome/CRC Institute). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
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Unpublished (1999)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                  /clone_lib="Wellcome CRC pRN3 St19 26"
/tissue_type="pooled embryos, stage 19-26"
/lab_host="DH108 (phage-resistant)"
/note="Vector: pBSRN3; Site 1: Not1; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library was constructed by N. Garrett, E. Bellefroid, and A.M. Zorn, (Wellcome/CRC Institute)."

[Wellcome/CRC Institute)."
                                                                                                                                                                                                                                                                                                 /db_xref="taxon:8355"
/clone="IMAGE:3550063"
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4.1%;
49.2%;
Score 44;
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26 Xenopus laevis cDNA clone
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                     Length 518;
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                                           190
  249 TTTGGATGAATCATTGGTTCGTGGTGTTACTGGTGATTTTGCATAGTTTTTGTTTCCTCAAG 308
                                                                                  - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuroyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Eukaryota, Bradopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP 191 91006 EVRY cedex -
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/clone_lib="RPCI-98"
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Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster The Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Drosophila melanogaster
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Ephydroidea, Drosophilidae, Drosophila.
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DNA linear GSS 26-JUL-19
survey sequence SP6 end of BAC
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                 ATGTCACAGAAAAAGAGGATAATGATGAAAACAATGATTCGCAGAAAGATTCAAAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          117;
              Plasmodium
BM276144
BM276144.1
                                    Texas A&M EST name:T258390e
TIGR sequence name:MTEBK36TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VandenBosch, K., Hurt, J.,
Town, C.D., Bowman, C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser, C.M.
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612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli strain XLOLR"
//note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagareishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library was constructed by R. Haywood, DNA sequencing Washington University Genome Sequencing Center For infoliations a clone please contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: L. David Sibley
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 527)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
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n quality sequence stop: 423.
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/lab_host="DH108 (GeneHog, Invitrogen, Inc.)"
/lab_host="DH108 (GeneHog, Invitrogen, Inc.)"
/note="wector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A) + RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene) clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH108 cells. Clone Availability: David Sibley, Washington University."
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/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA
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                                                                                                                                                                                                                                                                                                      TTTAGTTTTGGACTTGGGTCTCGGATTAACTCTCCCAGCCAACAAGAATGGTATTGC 926
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Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
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WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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WashU Plasmodium EST Project
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Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Liitu.
Tang, K., uillier, L., Martin, J., Wylie, T., Dante, M.,
Rennett, J., Jentes
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530 bp mRNA linear EST 20-DEC-2001
PfESToaa57c09.yl Plasmodium falciparum 3D7 gametocyte cDNA library
Plasmodium falciparum 3D7 cDNA 5', mRNA sequence.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Location/Qualifiers
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/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/note="Wector: pBluescript SK plus; Site_1: EcoRI; Site_2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A) + RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene) clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone Availability: David Sibley, Washington University."
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/db_xref="taxon:36329"
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                                                                                                    TTTGTGTGATGAAAAGCAAAAGGTTGCTGTTGAAGTTATCAAGAATTTATTGACTAATAC 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library was constructed by R. Haywood. DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley (sibley@borcim.wustl.edu), Washington University
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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//lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
//note="Vector: pBluescript SK plue; Site_1: EcoRI; Site_2:
XhoI; The library was constructed by R Haywood. cDNAs were
synthesized from ganetocyte poly(A) + RNA by oligo d(T)
priming, size-selected and directionally cloned into the
EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemid using the ExAssist helper phage
(Stratagene). Clones were mass excised using the ExAssist
helper phage (Stratagene), the phagemids were precitptated
with PEG 8000 and extracted with phenol/chloroform.
Phagemid DNA was electroporated into DH10B cells. Clone
Availability: David Sibley, Washington University."
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WashU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
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High quality sequence stop: 424.
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314 286 1810
                                                                    /dev stage="gametocyte (stage III-V)"
/lab_host="DH108 (GeneHog, Invitrogen, Inc.)"
/note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
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helper phage (Stratagene), the phagemids were precitptated
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phagemid DNA was electroporated into DH108 cells. Clone
Availability: David Sibley, Washington University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                library
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     4.18;
     Score 43.6;
     DB
     Length 570;
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                                                                                                         142;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL100640.1 GI:5612251
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genome sur
BACN06A03 of DrosBAC library from
                                                                                                                                                                                                                                                                                                                          project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/note="end : SP6"
47 c 28 g
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/clone_lib="DrosBAC"
                                                                                                                                                                                                                                                    organism="Drosophila melanogaster"
|db_xref="taxon:7227"
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38.0%;
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source
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Similarity

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Pred. No. 2.8; 1; Mismatches

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Search completed: January 27, 2003, 05:34:43 Job time: 1730 secs
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                                                                                                                                                                                                                                                                                                717 TATCATCAGAGATCAACAATACAATGTTCAACTCATTGGTACCTCTGATAAGCCCATACGT 776
                                                                                                                                                                                                                                                                                                                                                                 657 AGGTAAACCAATTTCAAACTACTATGTCGGATATAGTGAAAGTATGTGTGAAATTAAGGA 716
                                                                                                                                                                                                                                                                                                                                                                                                  783 TTHHYHHTTHYMHHTYMYHYYMYTCCYMCTYHCWHYYHTAYTCWTWTHHMWTWTHWYHH 842
                                                                                                                                                                                                                                                                                                                                                                                                                                   597 AACCATTTTGGATTCAACAGTTGTTGCCTCTCAAAGAGAATATATTAACTCTGTAAAGCA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AWWTTHTWWTHAYHWATYHYYYYMYCAMMCMCTHTCHHCYYYYHHYTAHHTHTHHWYAHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 CGGATTGTATCAACAATTACTCCAATCATCATCATCAGCTGCAGTTGATATCAAGGCCTC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    603 AHTTWYHWYHTYAMWHWITWHWIMWAWHWTTYTAAYYYYYTCWYYYHYMHWHHAHAHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 GGTTGGTTATGAACAAATTGTTTATCCAGATGTTGCCTCTTCTAGTTCTTTCACAGTTTT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722
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